Zagazig J. Agric. Res., Vol. 38 No. (4) 2011 813-824

GENE ACTION CONTROLLING YIELD, YIELD COMPONENTS AND OIL CONTENT IN CANOLA GENOTYPES (*BRASSICA NAPUS* L.)

Mohamed E. S. Kammoura*, A.H. Salem and H.A. Awaad

Agron. Dept., Fac. Agric., Zagazig University, Egypt.

ABSTRACT

Diallel cross among six rapeseed genotypes were used to study genetic behavior of yield components and oil content. The parents included Pactol, Serw 4, Serw 8, M 10, M 36 and M 39. This investigation was carried out at Kafr Abaza winter growing seasons 2006 /2007 and 2008 /2009. The obtained 15 F_1's together with the six parents were evaluated during 2008/2009 season in a randomized complete block design with three replicates. The results indicated that both additive and dominance genetic variances were highly significant for all studied characters except (H1) component for number of secondary branches/plant. Additive component played the major role in the inheritance of plant height, number of secondary branches/plant, number of silliquaes/plant, number of seeds/silliquae and seed oil content. Thus, phenotypic selection would be an effective procedure for improving these characters. Whereas, the dominance genetic variance was the main component controlling the inheritance of number of primary branches/plant and 1000-seed weight (g). The (KD/KR) ratio was more than unity for all studied characters except 1000-seed weight which was less than unity. The environmental variance was significant for yield contributing characters and seed oil content. Narrow sense heritability was high (> 50%) for all yield contributing characters, except 1000-seed weight which was moderate (42.1%).

Keywords: **Canola, diallel crosses, gene action, heritability, (*Brassica napus* L.).**

* **Corresponding author:** Mohamed E. S. Kammoura Tel.: +200125595291
E-mail address: Kammoura 1982@yahoo.com

INTRODUCTION

Canola crop is considered one of the most important sources for vegetables edible oils production in the world. Canola has less than 30 μg of glucosinolates per gram of oil-free meal and its seed meal can be used as a high-quality protein supplement for livestock (Bhardwaj, 2007). Canola having over 40% oil content is one of the highest oil-containing crops in the world. In Egypt, canola is of resent introduction but has a bright future and hopefully to contribute in reducing oil deficiency gap.

Separation out the total genetic variance to its main items additive and dominance gene effects using diallel analysis method was performed for yield and its components and seed oil content (%), in order to provide detailed genetic informations enable the breeder to choose the most efficient breeding methodology. Therefore, in the present study 6 x 6 diallel cross parents was further subjected to the second degree statistical analysis (Hayman, 1954 a and b) to test types of gene action controlling the studied characters.

In a study diallel cross analysis among six parental canola genotypes under different environment, El- Hosary *et al* (1999) found that additive and non-additive gene action controlled the expression of the genes for plant height, number of silliquaes/plant, number of seeds / silliquae and seed yield/ plant and the total genetic variability was due to the additive and additive x additive gene action in these traits. They recoded high heritability values for all the traits examined except for number of racemes / plant under low saline conditions and number of seeds /siliquae and seed index under high saline conditions. In continuous, Moreover, Sharaan *et al* (2007) evaluated six population of four canola crosses under low and high salinity levels and reveald that the parental differences in each cross were significant for number of branches, number of pods/plant, seed index, seed oil content and seed yield/plant. The results indicated that A, B and C scaling tests were significant in all crosses for all characters except for number pods/plant in cross (26/18 x drakkar). The dominance gene effect was significant for number of branches, number of pods/plant, seed index, seed oil content and seed yield/plant. The dxd interaction effect was positive and significant for number of branches/plant, number of pods/plant and seed yield/plant under both condition as well as seed oil content under low salinity level. Narrow sense heritability was high for number of branches/plant, number of pods/plant, seed oil content and varied from moderate to high for seed index and from low to high for seed yield/ plant under different conditions.

Furthermore, Amiri- Oghan *et al* (2009) computed genetic components of variance using twenty one F_2 progenies derived from a 7 ×7 diallel crosses along with parents for seed yield. They found that the Analysis of variance reveald that both additive and non-additive genetic effects were involved in controlling seed yield. Heritability in narrow sense was low (30.15%) for seed yield.

The present investigation aimed to identify types of gene action and heritability for rapeseed yield and its related characters as well as seed oil content using diallel cross analysis

MATERIALS AND METHODS

The present investigation was conducted at Kafr Abaza village, Zagazig district, Sharkia Governorate, Egypt, during the two successive winter growing seasons 2006 /2007 and 2007 /2008. In 2006 /2007 season six diverse rapeseed genotypes were selected and crossed in all possible combinations, excluding reciprocals to produce their F_1 crosses. Name and pedigree of the parental canola genotypes are shown in Table (1).

Table 1. Pedigree and origin of the six parental rapeseed genotypes used in the present study

Name	Pedigree	Origin
Pactol	Introduction cultivar	France
Serw 4	Producing in another culture	Local
Serw 8	Producing in another culture	Local
M 10*	Cresor variety treated with 200 Gry	Local
M 36*	Cresor variety treated with 200 Gry	Local
M 39*	Cresor variety treated with 200 Gry	Local

* The mutants that are used in this study were developed in previous, studies according to Sorour (1994) using Gamma radiations.

In 2007/2008 season, the six parental genotypes and their 15 F_1 crosses were evaluated in a randomized complete block design with three replications. Each cross was planted in a plot was 3.6 m^2 and consists of (2 rows for each parent + 2 rows for F_1 cross). The row length was 3m and 20cm apart. Plant to plant spacing was 10 cm. Ten guarded plants were chosen randomly from each parent and F_1 and the data of Plant height (cm), number of primary branches/plant, number of secondary branches/plant, number of silliques/plant, number of seeds/sillique, 1000-seed weight (g), seed yield/plant (g) were recorded. Seed oil content (%) was estimated according to A.O.A.C. (1980).

Analysis of variance was conducted to test the differences among various genotypes according to Snedecor and Cochran (1989). The diallel cross analysis adopted by Hyman (1954 a and b) was applied.

RESULTS AND DISCUSSION

Separating out the total genetic variance into its main components i.e. additive and dominance (H1 and H2) gene effects using the diallel analysis method was performed for yield and its components and seed oil content (%) in order to provide detailed genetic information for the breeder to choose the most efficient breeding methodology. Therefore, in the present study, the diallel analysis according to Hayman (1954 a and b) was used to identify the type of gene action controlling the studied characters.

Plant Height and Number of Branches / Plant

Data presented in Table 2 indicated that both additive (D) and dominance (H1&H2) genetic variances were highly significant for plant height, number of primary branches /plant and number of secondary branches /plant, except (H1)component for number of secondary branches/ plant. The additive genetic component was higher in its magnitudes as compared to the dominance one in controlling plant height, number of secondary branches, resulting in average degree of dominance less than unity, suggesting that the fixable gene type could be exploited through phenotypic selection. In this respect, additive and non additive gene action were found to be significant with the preponderance of additive gene action in controlling plant height by Aytac *et al* (2008) and Nassimi *et al* (2006).

The dominance genetic component was higher in its magnitudes as compared to the additive one in the inheritance of number of primary branches /plant, resulting in average degree of dominance more than unity, indicating that this character could be improved through hybrid breeding programs. Similar findings were obtained by Sharaan *et al* (2007) who showed that the dominance gene action was significant for number of branches / plant.

The covariance of additive and dominance gene effects in the parents (F value) was negative and significant for number of primary branches /plant, revealing that the decreasing alleles were more frequent than the increasing one in the parental population. Moreover the F value was positive and didn't reach the significance level for plant height and number of secondary branches /plant. The overall dominance effects of heterozygous loci (h^2) were negative and insignificant for plant height, number of secondary branches / plant, as well as positive and insignificant for number of primary branches /plant. The environmental value was significant for plant height and both primary and secondary branches /plant .This result indicates the influence of environmental conditions on these characters. The proportion of genes with positive and negative effects in the parents (H2/4H1) was less than its maximum value (0.25) for yield attributes, suggesting asymmetrical distribution of positive and negative alleles among the parental population. The proportion of dominance to recessive genes in the parents (KD / KR) was more than unity for the plant height, number of primary and secondary branches / plant indicated an excess of dominant alleles in the the parental genotypes. Narrow sense heritability was high (>50%) for plant height and branches / plant.

Table 2. Components of genetic variance and their derived parameters for plant height, number of primary branches /plant and number of secondary branches /plant using 6x6 diallel crosses of canola in F_1 generation

Genetic parameters	Plant height (cm)	Number of primary branches /plant	Number of secondary branches/plant
D	179.94**±	0.385**±	1.029**±
	16.17	0.072	0.255
H1	150.60**±	0.890**±	0.366**±
	13.801	0.98	0.187
H2	131.25**±	0.806**±	0.309*±
	11.28	0.086	0.139
F	12.89±	0.152*-±	0.349±
	14.56	0.062	0.264
h^2	-0.373±	0.025±	-0.009-±
	1.98	0.037	0.078
E	1.706**±	0.016**±	0.067**±
	0.269	0.002	0.011
Derived parameters			
H1/D	0.915**	1.520**	0.596**
H2/4H1	0.218**	0.226**	0.211**
KD/KR	316.379	1.148	1.1626
T(n)	0.730**	0.588**	0.718**

Thus selection may be operative for improving such characters. In this respect, high heritability was detected for plant height by Aytac *et al* (2008) and for number of branches / plant by Sharaan *et al* (2007).

Number of Silliquaes/ Plant, Number of Seeds/ Silliquae and 1000- Seed Weight

Data presented in Table 3 indicated that both additive (D) and dominance (H1&H2) genetic components were highly significant for number of silliquae / plant, number of seeds / silliquae and 1000 seed weight(g). The additive genetic component was higher in its magnitudes as compared to the dominance once, resulting in average degree of dominance less than unity. This result indicates that the fixable gene type could be exploited through phenotypic selection, In this respect, additive and non

Table 3. Component of genetic variance and their derived parameters for no. of silliquaes / plant, no. of seeds/silliquae and 1000-seed weight(gm) using 6x6 diallel crosses of canola in F_1 generation

Genetic parameters	No. of silliquaes/plant	No. of seeds/silliquae	1000-seed weight (g)
D	$409.70^{**\pm}$	$2.549^{**\pm}$	$0.150^{**\pm}$
	50.58	0.366	0.27
H1	$92.01^{**\pm}$	$0.459^{*\pm}$	$0.248^{**\pm}$
	27.34	0.182	0.34
H2	$65.73^{**\pm}$	$0.430^{**\pm}$	$0.206^{**\pm}$
	18.34	0.151	0.027
F	$179.65^{**\pm}$	$0.340^{\pm}$	$0.108^{**\pm}$
	51.32	0.327	0.033
h^2	$-1.763^{\pm}$	$0.042^{\pm}$	$0.042^{\pm}$
	8.211	0.122	0.024
E	$7.43^{**\pm}$	$0.066^{**\pm}$	$0.005^{**\pm}$
	1.20	0.010	0.0009
Derived parameters			
H1/D	0.474**	0.425**	1.288**
H2/4H1	0.179**	0.234**	0.208**
KD/KR	209.123	1.98	0.557
T(n)	0.843**	0.866**	0.421*

additive gene action were found to be significant with the preponderance of additive gene action in controlling the foregoing characters by El-Hosary *et al* (1999) and Zhao *et al* (2009).

The dominance genetic component was higher in its magnitudes as compared to the additive one in the inheritance of 1000 seed weight, resulting in average degree of dominance more than unity, indicating that this character could improved through hybrid breeding programs. Similar finding was obtained under low salinity by Sharaan *et al* (2007).

The covariance of additive and dominance gene effects in the parents (F value) were positive and highly significant for number of silliquaes / plant, 1000- seed weight, indicating more frequent of the increasing dominance alleles than recessive one in the parental population.

Moreover, the F value was positive but didn't reach the significance for number of seeds / silliquae. The overall dominance affects of heterozygous loci (h^2) were negative and insignificant for number of silliquaes / plant as well as positive and insignificant for number of seeds / silliquae. The environmental value was significant for the foregoing yield components .This result indicates the influence of environmental conditions on the studied characters.

The proportion of genes with positive and negative effects in the parents (H2/4H1) was less than its maximum value (0.25) for yield attributes, suggesting asymmetrical distribution of positive and negative alleles among the parental population. The proportion of dominance to recessive genes in the parents (KD / KR) was more than unity for the studied number of silliquaes/plant, and number of seeds/silliquae, indicating an excess of dominant alleles in the parental genotypes. Otherwise, (KD / KR) ratio was less than unity for 1000-seed weight, revealing an excess of recessive alleles than dominant once in the parental populations.

Narrow sense heritability was moderate (42.1%) for 1000-seed weight and high (>50%) for number of silliquaes /plant and number of seeds / silliquae.

Thus selection may be operative for improving such characters. In this regard, moderate to high narrow sense heritability was detected for such yield attributes (El-Hosary *et al*, (1999) , Sharaan *et al*, (2007) and Zhao *et al*, (2009).

Seed Yield/Plant and Seed Oil Content (%)

Data presented in Table 4 indicated that both additive (D) and dominance (H1&H2) genetic variances were highly significant for seed yield/plant. Therefore, pedigree method could be exploited for improving seed yield. Whereas, additive genetic variance was the main component controlling seed oil content. In this respect, additive and non additive gene action were found to be significant with the preponderance of additive gene action in controlling seed yield and seed oil

Table 4. Component of genetic variance and their derived parameters for seed yield/plant and seed oil content (%) using 6x6 diallel crosses of canola in F_1 generation

Genetic parameters	Seed yield/plant (g)	Seed oil content (%)
D	1.165**±	5.555**±
	0.119	0.267
H1	0.846**±	1.115±
	0.092	0.731
H2	0.756**±	0.656±
	0.078	0.654
F	0.323**±	0.042±
	0.117	0.698
h^2	0.591±	-0.208±
	0.139	0.44
E	0.015**±	0.792**±
	0.002	0.007
Derived parameters		
H1/D	0.852**	0.448
H2/4H1	0.223**	0.147
KD/KR	1.824	4.943
T(n)	0.695**	75.74

content by Sharaan *et al*(2007) who showed that additive x additive interaction effect was significant for seed yield /plant and seed oil content under low salinity level. Furthermore, Amiri- Oghan *et al* (2009) found that additive and non- additive genetic effects were involved in controlling seed yield with low narrow sense heritability.

The covariance of additive and dominance gene effects in the parents (F value) was positive and significant for seed yield /plant, revealing that the decreasing alleles were more frequent than the increasing one in the parental population. Moreover the F value was positive and didn't reach the significance level for seed oil content. The overall dominance effects of heterozygous loci (h^2) were positive and insignificant for seed yield /plant, as well as negative and insignificant for seed oil content(%).The environmental value was significant for both characters. This result indicates the influence of environmental conditions on both characters.

The proportion of genes with positive and negative effects in the parents (H2/4H1) was less than its maximum value (0.25), suggesting asymmetrical distribution of positive and negative alleles among the parental population. The proportion of dominance to recessive genes in the parents (KD / KR) was more than unity for the seed yield plant and seed oil content indicating an excess of dominant alleles than recessive ones in the parents.

Narrow sense heritability was high (>50%) for the studied characters. These results indicate that phenotypic selection may be operative for improving such characters. In this respect, high heritability was detected for seed oil content and low for seed yield / plant by Sharaan *et al*. (2007). Whereas, high heritability was registered for seed yield / plant coupled with genetic advance by Aytac *et al* (2008) and Zhao *et al*, (2009).

REFERENCES

Amiri–Oghan, H., M.H. Fotokian, F. Javidfar and B. Alizaeh (2009). Genetic analysis of grain yield, days to flowering and maturity in oilseed rape (*Brassica napus* L.) using diallel crosses. International J. of Plant production, 3(2):19-26.

A.O.A.C. (1980). Association of Official Agriculture Chemist. Official method of analysis. 13th d., Washington D.C., USA.

Aytac, Z., G. Knac and E. Knac (2008). Genetic variation, heritability and path analysis of summer rapeseed cultivars .J. of Applaw 3541. Biological – Sci., 2(3): 35-39.

Bhardwaj, H.L. (2007). Utilizing locally – produced canola to manufacture biodiesel. In: J. Janick and A. Whipkey, Editors, *Issues* in New Crops and New Uses, ASHS press, Alexandria, VA. PP.43-46.

El-Hosary, A.A., S.A.N Afiah, M.EL. Badawy and A.I. Hassan (1999). Diallel cross analysis of canola (*Brassica napus* L.) under different environments. Annals of Agric. Sci., Moshtohor, 37 (1): 97-112.

Hayman, B.I. (1954a). the analysis of variance of diallel tables. Biometrics, 10:235-244.

Hayman, B.I. (1954 b). The theory and analysis of diallel crosses. Genetics, 39:789-809.

Nassimi, A.W., S.A. Raziuddin, H. Ghulam and A. Naushed (2006). Combining ability analysis for maturity and other traits in rapeseed (*Brassica napus* L.). J. of Agron.,5(3): 523-526.

Sharaan, A.N., K.H. Ghallab and A.E. S.Khalaf (2007). Variability, gene effects and genetic parameters in six populations of four canola crosses as affected by different levels of soil salinity. Egyptian J. Plant Breed., 11 (1):281-299.

Snedecor, G.W. and W.G. Cochran (1989). Statical Methods, 8th ed. Iowa State, Univ. Press Iowa, USA.

Sorour, W.A. (1994). Meiotic abnormalities and useful mutant behavior in irradiated oil rapeseed. Egypt. J. Genet. Cytology, 24: 75 – 84.

Zhao, Y., L. Xiao and L.V. Chang-ming (2009). Genetic analysis of yield and its components of *B. napus* hybrid using Resynthesized rapeseed lines. Agric. Sci. in China, 8(11): 1286-1292.

الفعل الجينى المتحكم فى المحصول ومكوناته ومحتوى الزيت فى الكانولا

محمد السيد سعيد قمورة – عبدالحميد حسن سالم– حسن عودة عواد

قسم المحاصيل– كلية الزراعة– جامعة الزقازيق– مصر

أجريت هذه الدراسة بحقل إرشادى بقرية كفر أباظــة–الزقازيق– محافظة الشرقية خلال موسمى ٢٠٠٦/ ٢٠٠٧ و ٢٠٠٧/ ٢٠٠٨بهدف دراسة الفعــل الجينــى المــتحكم فــى المحصول ومكوناته ومحتوى البذرة من الزيت(%) فى محصول الكانولا وذلــك باســتخدام الجيل الأول الناتج من تهجين ستة تراكيب وراثية من الكانولا متباينة فى صفاتها بطريقــة الدياليل واشتملت التراكيب الأبوية على الأصناف بكتول، سرو٤، سرو٨ وثــلاث ســلالات هى M10 ،M 36 ،M 39.

وأشارت النتائج إلى معنوية كل من الفعل الجينى والسيادى فى وراثة جميع الصفات تحت الدراسة ماعدا عدد الأفرع الثانوية للنبات ولعب المكون المضيف الدور الرئيسى فى وراثة صفات ارتفاع النبات ، عدد الأفرع الثانوية للنبات، عدد الخرادل للنبات، عدد بذور الخردلة، محصول البذور للنبات ومحتوى البذرة من الزيت، مشيرا إلى فاعلية الانتخاب المظهرى فى وراثة هذه الصفات. بينما لعب الفعل الجينى السيادى الدور الأكبر فى وراثة صفتى عدد الأفرع الأولية للنبات ووزن الألف بذرة وبالتالى يمكن تحسينها عن طريق التهجين.

كانت النسبة (H2/4H1) اقل من القيمة القصوى لها فى جميع الصفات المدروسة، مما يشير إلى التوزيع غير المتماثل للآليلات الموجبة والسالبة بين الآباء لهذه الصفات. وكانت نسبة(KD/KR) أكبر من الوحدة لجميع الصفات المدروسة ماعدا وزن الألف بذرة حيث كانت اقل من الوحدة.

كان التباين البيئى معنويا فى تأثيره على الصفات المدروسة. و كانت قيم كفاءة التوريث بالمعنى الضيق عالية (أكبر من ٥٠%) لكل الصفات تحت الدراسة ماعدا وزن الآلف بذرة حيث كانت متوسطة (٤٢,١ %).